

IN THE SPECIFICATION

Please replace paragraph on page 8, beginning at line 18, with the following paragraph:

Table 1 Primers used to determine nucleotide sequence of 18s rRNA gene (forward direction)

<u>Sequence No.</u> <u>SEQ ID NO:</u>	Name	Sequence
1	NS1	5'-gtagtcataatgcttgtct-3'
2	NS3	5'-gcaaggctggtgccagcagcc-3'
3	NS5	5'-aacttaaaggaaattgacggaag-3'
4	NS7	5'-gaggcaataacaggctgtgatg-3'

Please replace paragraph on page 8, beginning at line 26, with the following paragraph:

Table 2 Primers used to determine nucleotide sequence of 18s rRNA gene (reverse direction)

<u>Sequence No.</u> <u>SEQ ID NO:</u>	Name	Sequence
5	NS2	5'-cggtcagaccacggcgtcg-3'
6	NS4	5'-ttgaatttccttaactgccttc-3'
7	NS6	5'-ctccgttattgtccagacactac-3'
8	NS8	5'-aggcatccacttggacgcct-3'

Please replace paragraph on page 9, beginning at line 8, with the following paragraph:

The DNA sequence of a known strain was obtained from Japan DNA Data Bank (<http://www.ddbj.nig.ac.jp/> www.ddbj.nig.ac.jp/) to examine the homology of the 18S rRNA genes. As a result, this 18S rRNA gene had 99% (upstream 803 bases) homology with the 18S rRNA gene of Mortierella hyalina (GenBank, accession no. AY157493), 98% (full length) homology with the 18S rRNA gene of Mortierella chlamydospora (GenBank accession No. AF157143) and 98% (full length) homology with the 18S rRNA gene of Mortierella multidivaricata (GenBank accession No. AF157144).

Please replace paragraph on page 10, beginning at line 18, with the following paragraph:

The DNA sequence of a known strain was obtained from Japan DNA Data Bank (<http://www.ddbj.nig.ac.jp/> www.ddbj.nig.ac.jp/) to examine the homology of the 18S rRNA genes. As a result, this 18S rRNA gene had 100% (upstream 803 bases) homology with the 18S rRNA gene of Mortierella hyalina (GenBank, accession no. AY157493), 98% (full length) homology with the 18S rRNA gene of Mortierella chlamydospora (GenBank accession No. AF157143) and 98% (full length) homology with the 18S rRNA gene of Mortierella multidivaricata (GenBank accession No. AF157144).

Please replace paragraph on page 22, beginning at line 5, with the following paragraph:

The DNA sequences of known strains were obtained from Japan DNA Data Bank (<http://www.ddbj.nig.ac.jp/> www.ddbj.nig.ac.jp/) to examine the homology of 400 to 500 bases on the 5' terminal side of the 16s rRNA genes. As a result, this 16s rRNA gene had 98% homology with the 16s rRNA gene of *Micromonospora* sp. DSM44396 (GenBank, accession no. AJ560637), 98% homology with a gene of *Micromonospora purpureochromogenes* (GenBank accession No. X92611), 95% homology with a gene of *M. Chalcea* IFO12135 (GenBank, accession no. D85489) which is a type strain of genus *Micromonospora* and 95% homology with a gene of *Verrucosispora giphornensis* (GenBank, accession no. Y15523) which is a type strain of genus *Verrucosispora*.